

SEQUENCE LISTING

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<120> A Novel Ligand For FPRL1 And Its Use

<130> 3118 USOP

<140> US/10/534,082

<141> 2005-05-05

<150> PCT/JP2003/014138

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<150> JP 2002-324189

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<150> JP 2002-367119

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<213> Homo sapiens

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35 40 45

Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Thr Thr Ile Cys Tyr
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Leu Ile Val Ser Met Ala Met Gly Glu Lys Trp Pro Phe Gly Trp Phe
85 90 95

Leu Cys Lys Leu Ile His Ile Val Val Asp Ile Asn Leu Phe Gly Ser
100 105 110

Val Phe Leu Ile Gly Phe Ile Ala Leu Asp Arg Cys Ile Cys Val Leu
115 120 125

His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Met Lys
130 135 140

Val Ile Val Gly Pro Trp Ile Leu Ala Leu Val Leu Thr Leu Pro Val
145 150 155 160

Phe Leu Phe Leu Thr Thr Val Thr Ile Pro Asn Gly Asp Thr Tyr Cys
165 170 175

Thr Phe Asn Phe Ala Ser Trp Gly Gly Thr Pro Glu Glu Arg Leu Lys
180 185 190

Val Ala Ile Thr Met Leu Thr Ala Arg Gly Ile Ile Arg Phe Val Ile
195 200 205

Gly Phe Ser Leu Pro Met Ser Ile Val Ala Ile Cys Tyr Gly Leu Ile
210 215 220

Ala Ala Lys Ile His Lys Lys Gly Met Ile Lys Ser Ser Arg Pro Leu
225 230 235 240

Arg Val Leu Thr Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro
 245 250 255

Phe Gln Leu Val Ala Leu Leu Gly Thr Val Trp Leu Lys Glu Met Leu
 260 265 270

Phe Tyr Gly Lys Tyr Lys Ile Ile Asp Ile Leu Val Asn Pro Thr Ser
 275 280 285

Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Val Phe
 290 295 300

Val Gly Gln Asp Phe Arg Glu Arg Leu Ile His Ser Leu Pro Thr Ser
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 tat gag tct gct ggc tac act gtt ctg cgg atc ctc cca ttg gtg gtg 96
 Tyr Glu Ser Ala Gly Tyr Thr Val Leu Arg Ile Leu Pro Leu Val Val
 20 25 30
 ctt ggg gtc acc ttt gtc ctc ggg gtc ctg ggc aat ggg ctt gtg atc 144
 Leu Gly Val Thr Phe Val Leu Gly Val Leu Gly Asn Gly Leu Val Ile
 35 40 45
 tgg gtg gct gga ttc cgg atg aca cgc aca gtc acc acc atc tgt tac 192
 Trp Val Ala Gly Phe Arg Met Thr Arg Thr Val Thr Thr Ile Cys Tyr
 50 55 60
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Leu Ile Val Ser Met Ala Met Gly Glu Lys Trp Pro Phe Gly Trp Phe	
85 90 95	
ctg tgt aag tta att cac atc gtg gtg gac atc aac ctc ttt gga agt	336
Leu Cys Lys Leu Ile His Ile Val Val Asp Ile Asn Leu Phe Gly Ser	
100 105 110	
gtc ttc ttg att ggt ttc att gca ctg gac cgc tgc att tgt gtc ctg	384
Val Phe Leu Ile Gly Phe Ile Ala Leu Asp Arg Cys Ile Cys Val Leu	
115 120 125	
cat cca gtc tgg gcc cag aac cac cgc act gtg agt ctg gcc atg aag	432
His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Met Lys	
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Val Ile Val Gly Pro Trp Ile Leu Ala Leu Val Leu Thr Leu Pro Val	
145 150 155 160	
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Phe Leu Phe Leu Thr Thr Val Thr Ile Pro Asn Gly Asp Thr Tyr Cys	
165 170 175	
act ttc aac ttt gca tcc tgg ggt ggc acc cct gag gag agg ctg aag	576
Thr Phe Asn Phe Ala Ser Trp Gly Gly Thr Pro Glu Glu Arg Leu Lys	
180 185 190	
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Val Ala Ile Thr Met Leu Thr Ala Arg Gly Ile Ile Arg Phe Val Ile	
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Gly Phe Ser Leu Pro Met Ser Ile Val Ala Ile Cys Tyr Gly Leu Ile	
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gca gcc aag atc cac aaa aag ggc atg att aaa tcc agc cgt ccc tta	720
Ala Ala Lys Ile His Lys Lys Gly Met Ile Lys Ser Ser Arg Pro Leu	
225 230 235 240	
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245 250 255	
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Phe Gln Leu Val Ala Leu Leu Gly Thr Val Trp Leu Lys Glu Met Leu	
260 265 270	
ttc tat ggc aag tac aaa atc att gac atc ctg gtt aac cca acg agc	864
Phe Tyr Gly Lys Tyr Lys Ile Ile Asp Ile Leu Val Asn Pro Thr Ser	
275 280 285	
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Ser Leu Ala Phe Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Val Phe	

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Val Gly Gln Asp Phe Arg Glu Arg Leu Ile His Ser Leu Pro Thr Ser			
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Leu Glu Arg Ala Leu Ser Glu Asp Ser Ala Pro Thr Asn Asp Thr Ala			
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Leu Ser Ile Thr Phe Val Leu Gly Val Leu Gly Asn Gly Leu Val Ile			
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Trp Val Ala Gly Phe Arg Met Val His Thr Val Thr Thr Cys Phe			
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Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Thr Val Thr Leu Pro Phe			
	65	70	75
Phe Val Ile Ser Ile Ala Met Lys Glu Lys Trp Pro Phe Gly Trp Phe			
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Leu Cys Lys Leu Val His Ile Val Val Asp Ile Asn Leu Phe Gly Ser			
	100	105	110
Val Phe Leu Ile Ala Leu Ile Ala Leu Asp Arg Cys Ile Cys Val Leu			
	115	120	125
His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Arg Lys			
	130	135	140
Val Val Val Gly Pro Trp Ile Leu Ala Leu Ile Leu Thr Leu Pro Ile			
	145	150	155
Phe Ile Phe Met Thr Thr Val Arg Ile Pro Gly Gly Asn Val Tyr Cys			
	165	170	175
Thr Phe Asn Phe Ala Ser Trp Gly Asn Thr Ala Glu Glu Leu Leu Asn			
	180	185	190
Ile Ala Asn Thr Phe Val Thr Val Arg Gly Ser Ile Arg Phe Ile Ile			
	195	200	205
Gly Phe Ile Met Pro Met Ser Ile Val Ala Ile Cys Tyr Gly Leu Ile			
	210	215	220
Ala Val Lys Ile His Arg Arg Ala Leu Val Asn Ser Ser Arg Pro Leu			
	225	230	235
Arg Val Leu Thr Ala Val Val Ala Ser Phe Phe Ile Cys Trp Phe Pro			
	245	250	255
Phe Gln Leu Val Ala Leu Leu Gly Thr Ile Trp Phe Lys Glu Ser Leu			
	260	265	270
Phe Ser Gly Arg Tyr Lys Ile Leu Asp Met Trp Val His Pro Thr Ser			
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Ser Leu Ala Tyr Phe Asn Ser Cys Leu Asn Pro Met Leu Tyr Ala Phe			

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Met Gly Gln Asp Phe His Glu Arg Leu Ile His Ser Leu Pro Ser Ser				
305		310		315
Leu Glu Arg Ala Leu Ser Glu Asp Ser Gly Gln Thr Ser Asp Thr Gly				
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Val Ser Ile Thr Phe Phe Leu Gly Val Leu Gly Asn Gly Leu Val Ile					
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Trp Val Ala Gly Phe Arg Met Pro His Thr Val Thr Thr Ile Trp Tyr					
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Leu Asn Leu Ala Leu Ala Asp Phe Ser Phe Thr Ala Thr Leu Pro Phe					
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Leu Leu Val Glu Met Ala Met Lys Glu Lys Trp Pro Phe Gly Trp Phe					
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Leu Cys Lys Leu Val His Ile Val Val Asp Val Asn Leu Phe Gly Ser					
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Val Phe Leu Ile Ala Leu Ile Ala Leu Asp Arg Cys Ile Cys Val Leu					
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His Pro Val Trp Ala Gln Asn His Arg Thr Val Ser Leu Ala Arg Lys					
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Leu	Glu	Arg	Ala	Leu	Ser	Glu	Asp	Ser	Gly	Gln	Thr	Ser	Asp	Ser	Ser
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Thr	Ser	Ser	Thr	Ser	Pro	Pro	Ala	Asp	Ile	Glu	Leu	Lys	Ala	Pro	
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ctctatgttt tcatgggcca ggactttcgt gagagattta ttcattccct gccttatagt	960
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